

## SEQUENCE LISTING

&lt;110&gt; W. James Jackson

&lt;120&gt; CHLAMYDIA PROTEIN, GENE SEQUENCE AND USES THEREOF

&lt;130&gt; 7969-087

&lt;160&gt; 71

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 2898

&lt;212&gt; DNA

&lt;213&gt; Chlamydia sp

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) . . . (2895)

&lt;400&gt; 1

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Met	Lys	Lys	Ala	Phe	Phe	Phe	Phe	Leu	Ile	Gly	Asn	Ser	Leu	Ser	Gly		
1			5					10					15				

c	ta	gct	aga	gag	gtt	cct	tct	aga	atc	ttt	ctt	atg	ccc	aac	tca	gtt		96
Leu	Ala	Arg	Glu	Val	Pro	Ser	Arg	Ile	Phe	Leu	Met	Pro	Asn	Ser	Val			
				20				25					30					

cca	gat	cct	acg	aaa	gag	tcg	cta	tca	aat	aaa	att	agt	ttg	aca	gga		144
Pro	Asp	Pro	Thr	Lys	Glu	Ser	Leu	Ser	Asn	Lys	Ile	Ser	Leu	Thr	Gly		
				35				40				45					

gac	act	cac	aat	ctc	act	aac	tgc	tat	ctc	gat	aac	cta	cgc	tac	ata		192
Asp	Thr	His	Asn	Leu	Thr	Asn	Cys	Tyr	Leu	Asp	Asn	Leu	Arg	Tyr	Ile		
				50				55				60					

ctg	gct	att	cta	caa	aaa	act	ccc	aat	gaa	gga	gct	gct	gtc	aca	ata		240
Leu	Ala	Ile	Leu	Gln	Lys	Thr	Pro	Asn	Glu	Gly	Ala	Ala	Val	Thr	Ile		
				65				70			75		80				

aca	gat	tac	cta	agc	ttt	ttt	gat	aca	caa	aaa	gaa	ggt	att	tat	ttt		288
Thr	Asp	Tyr	Leu	Ser	Phe	Phe	Asp	Thr	Gln	Lys	Glu	Gly	Ile	Tyr	Phe		
				85				90			95						

gca	aaa	aat	ctc	acc	cct	gaa	agt	ggt	ggt	gcg	att	ggt	tat	gct	agt		336
Ala	Lys	Asn	Leu	Thr	Pro	Glu	Ser	Gly	Gly	Ala	Ile	Gly	Tyr	Ala	Ser		
				100				105			110						

ccc	aat	tct	cct	acc	gtg	gag	att	cgt	gat	aca	ata	ggt	cct	gta	atc		384
Pro	Asn	Ser	Pro	Thr	Val	Glu	Ile	Arg	Asp	Thr	Ile	Gly	Pro	Val	Ile		
				115				120			125						

ttt	gaa	aat	aat	act	tgt	tgc	aga	cca	ttt	aca	tgc	agt	aat	cct	aat		432
Phe	Glu	Asn	Asn	Thr	Cys	Cys	Arg	Pro	Phe	Thr	Ser	Ser	Asn	Pro	Asn		
				130				135			140						

gca gct gtt aat aaa ata aga gaa ggc gga gcc att cat gct caa aat Ala Ala Val Asn Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn 145 150 155 160	480
ctt tac ata aat cat aat cat gat gtg gtc gga ttt atg aag aac ttt Leu Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe 165 170 175	528
tct tat gtc cga gga gga gcc att agt acc gct aat acc ttt gtt gtg Ser Tyr Val Arg Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val 180 185 190	576
agc gag aat cag tct tgt ttt ctc ttt atg gac aac atc tgt att caa Ser Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln 195 200 205	624
act aat aca gca gga aaa ggt ggc gct atc tat gct gga acg agc aat Thr Asn Thr Ala Gly Lys Gly Ala Ile Tyr Ala Gly Thr Ser Asn 210 215 220	672
tct ttt gag agt aat aac tgc gat ctc ttc ttt atc aat aac gcc tgt Ser Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys 225 230 235 240	720
tgt gca gga gga gcg atc ttc tcc cct atc tgt tct cta aca gga aat Cys Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn 245 250 255	768
cgt ggt aac atc gtt ttc tat aac aat cgc tgc ttt aaa aat gta gaa Arg Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu 260 265 270	816
aca gct tct tca gaa gct tct gat gga gga gca att aaa gta act act Thr Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr 275 280 285	864
cgc cta gat gtt aca ggc aat cgt ggt agg atc ttt ttt agt gac aat Arg Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn 290 295 300	912
atc aca aaa aat tat ggc gga gct att tac gct cct gta gtt acc cta Ile Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu 305 310 315 320	960
gtg gat aat ggc cct acc tac ttt ata aac aat atc gcc aat aat aag Val Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys 325 330 335	1008
ggg ggc gct atc tat ata gac gga acc agc aac tcc aaa att tct gcc Gly Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala 340 345 350	1056
gac cgc cat gct att att ttt aat gaa aat att gtg act aat gta act Asp Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr 355 360 365	1104

aat gca aat ggt acc agt acg tca gct aat cct cct aga aga aat gca Asn Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala	370	375	380	1152	
ata aca gta gca agc tcc tct ggt gaa att cta tta gga gca ggg agt Ile Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser	385	390	395	400	1200
agc caa aat tta att ttt tat gat cct att gaa gtt agc aat gca ggg Ser Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly	405		410	415	1248
gtc tct gtg tcc ttc aat aag gaa gct gat caa aca ggc tct gta gta Val Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val	420	425		430	1296
ttt tca gga gct act gtt aat tct gca gat ttt cat caa cgc aat tta Phe Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu	435	440	445		1344
caa aca aaa aca cct gca ccc ctt act ctc agt aat ggt ttt cta tgt Gln Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys	450	455	460		1392
atc gaa gat cat gct cag ctt aca gtg aat cga ttc aca caa act ggg Ile Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly	465	470	475	480	1440
ggg gtt gtt tct ctt ggg aat gga gca gtt ctg agt tgc tat aaa aat Gly Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn	485	490		495	1488
ggg gca gga aat tct gct agc aat gcc tct ata aca ctg aag cat att Gly Ala Gly Asn Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile	500	505		510	1536
gga ttg aat ctt tct tcc att ctg aaa agt ggt gct gag att cct tta Gly Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu	515	520	525		1584
ttg tgg gta gag cct aca aat aac agc aat aac tat aca gca gat act Leu Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr	530	535	540		1632
gca gct acc ttt tca tta agt gat gta aaa ctc tca ctc att gat gac Ala Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp	545	550	555	560	1680
tat ggg aat tct cct tat gaa tcc aca gat cta acc cat gct ctg tca Tyr Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser	565	570		575	1728
tca cag cct atg cta tct att tct gag gct agt gat aac cag cta aga Ser Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Arg	580	585		590	1776

tct gat gat atg gat ttt tcg gga cta aat gtc cct cat tat gga tgg Ser Asp Asp Met Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp 595 600 605	1824
caa gga ctt tgg act tgg ggc tgg gca aaa act caa gat cca gaa cca Gln Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro 610 615 620	1872
gca tct tca gca aca atc aca gat cca caa aaa gcc aat aga ttc cat Ala Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His 625 630 635 640	1920
aga acc tta tta ctg act tgg ctt cct gct ggg tat gtt cct agc ccg Arg Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro 645 650 655	1968
aaa cac aga agt ccc ctc ata gcg aat acc tta tgg ggg aat atg ctg Lys His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu 660 665 670	2016
ctt gca aca gaa agc tta aaa aat agt gca gaa ctg aca cct agt gat Leu Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Asp 675 680 685	2064
cat cct ttc tgg gga att aca gga gga gga cta ggc atg atg gtt tac His Pro Phe Trp Gly Ile Thr Gly Gly Leu Gly Met Met Val Tyr 690 695 700	2112
caa gat cct cga gaa aat cat cct gga ttc cat atg cgc tct tcc gga Gln Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly 705 710 715 720	2160
tac tct gcg ggg atg ata gca ggg cag aca cac acc ttc tca ttg aaa Tyr Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys 725 730 735	2208
ttc agt cag acc tac acc aaa ctc aat gag cgt tac gca aaa aac aac Phe Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn 740 745 750	2256
gta tct tct aaa aat tac tca tgc caa gga gaa atg ctc ttc tca ttg Val Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu 755 760 765	2304
caa gaa ggt ttc ttg ctg act aaa tta gtt ggg ctt tac agc tat gga Gln Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly 770 775 780	2352
gac cat aac tgt cac cat ttc tat acc caa gga gaa aat cta aca tct Asp His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser 785 790 795 800	2400
caa ggg acg ttc cgt agt caa acg atg gga ggt gct gtt ttt ttt gat Gln Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp 805 810 815	2448

ctc cct atg aaa ccc ttt gga tca acg cat ata ctg aca gct ccc ttt Leu Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe 820 825 830	2496
tta ggt gct ctt ggt att tat tct agc ctg tct cac ttt act gag gtg Leu Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val 835 840 845	2544
gga gcc tat ccg cga agc ttt tct aca aag act cct ttg atc aat gtc Gly Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val 850 855 860	2592
cta gtc cct att gga gtt aaa ggt agc ttt atg aat gct acc caa aga Leu Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr Gln Arg 865 870 875 880	2640
cct caa gcc tgg act gta gaa ttg gca tac caa ccc gtt ctg tat aga Pro Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg 885 890 895	2688
caa gaa cca ggg atc gcg acc cag ctc cta gcc agt aag ggt att tgg Gln Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp 900 905 910	2736
ttt ggt agt gga agc ccc tca tcg cgt cat gcc atg tcc tat aaa atc Phe Gly Ser Gly Ser Pro Ser Arg His Ala Met Ser Tyr Lys Ile 915 920 925	2784
tca cag caa aca caa cct ttg agt tgg tta act ctc cat ttc cag tat Ser Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr 930 935 940	2832
cat gga ttc tac tcc tct tca acc ttc tgt aat tat ctc aat ggg gaa His Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu 945 950 955 960	2880
att gct ctg cga ttc tag Ile Ala Leu Arg Phe 965	2898
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Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly 35 40 45	
Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile 50 55 60	
Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile 65 70 75 80	

Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe  
                   85                  90                  95  
 Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser  
                   100              105                  110  
 Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile  
                   115              120                  125  
 Phe Glu Asn Asn Thr Cys Cys Arg Pro Phe Thr Ser Ser Asn Pro Asn  
                   130              135                  140  
 Ala Ala Val Asn Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn  
                   145              150                  155                  160  
 Leu Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe  
                   165              170                  175  
 Ser Tyr Val Arg Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val  
                   180              185                  190  
 Ser Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln  
                   195              200                  205  
 Thr Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn  
                   210              215                  220  
 Ser Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys  
                   225              230                  235                  240  
 Cys Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn  
                   245              250                  255  
 Arg Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu  
                   260              265                  270  
 Thr Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr  
                   275              280                  285  
 Arg Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn  
                   290              295                  300  
 Ile Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu  
                   305              310                  315                  320  
 Val Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys  
                   325              330                  335  
 Gly Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala  
                   340              345                  350  
 Asp Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr  
                   355              360                  365  
 Asn Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala  
                   370              375                  380  
 Ile Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser  
                   385              390                  395                  400  
 Ser Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly  
                   405              410                  415  
 Val Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val  
                   420              425                  430  
 Phe Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu  
                   435              440                  445  
 Gln Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys  
                   450              455                  460  
 Ile Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly  
                   465              470                  475                  480  
 Gly Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn  
                   485              490                  495  
 Gly Ala Gly Asn Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile  
                   500              505                  510  
 Gly Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu  
                   515              520                  525  
 Leu Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr  
                   530              535                  540

Ala Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp  
 545 550 555 560  
 Tyr Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser  
 565 570 575  
 Ser Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Arg  
 580 585 590  
 Ser Asp Asp Met Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp  
 595 600 605  
 Gln Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro  
 610 615 620  
 Ala Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His  
 625 630 635 640  
 Arg Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro  
 645 650 655  
 Lys His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu  
 660 665 670  
 Leu Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Asp  
 675 680 685  
 His Pro Phe Trp Gly Ile Thr Gly Gly Leu Gly Met Met Val Tyr  
 690 695 700  
 Gln Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly  
 705 710 715 720  
 Tyr Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys  
 725 730 735  
 Phe Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn  
 740 745 750  
 Val Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu  
 755 760 765  
 Gln Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly  
 770 775 780  
 Asp His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser  
 785 790 795 800  
 Gln Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp  
 805 810 815  
 Leu Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe  
 820 825 830  
 Leu Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val  
 835 840 845  
 Gly Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val  
 850 855 860  
 Leu Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr Gln Arg  
 865 870 875 880  
 Pro Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg  
 885 890 895  
 Gln Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp  
 900 905 910  
 Phe Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile  
 915 920 925  
 Ser Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr  
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 His Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu  
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1					5					10					15		

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Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu Gly Glu Thr Ala

20 25 30

ctc ctc act aaa aat cct aat cat gtc gtc tgt aca ttt ttt gag gac

Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe Glu Asp

35 40 45

tgt acc atg gag agc ctc ttt cct gct ctt tgt gct cat gca tca caa

Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala Ser Gln

50 55 60

gac gat cct ttg tat gta ctt gga aat tcc tac tgt tgg ttc gta tct

Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe Val Ser

65 70 75 80

aaa ctc cat atc acg gac ccc aaa gag gct ctt ttt aaa gaa aaa gga

Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu Lys Gly

85 90 95

gat ctt tcc att caa aac ttt cgc ttc ctt tcc ttc aca gat tgc tct

Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp Cys Ser

100 105 110

tcc aag gaa agc tct cct tct att att cat caa aag aat ggt cag tta

Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly Gln Leu

115 120 125

tcc ttg cgc aat aat ggt agc atg agt ttc tgt cga aat cat gct gaa

Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His Ala Glu

130 135 140

ggc tct gga gga gcc atc tct gcg gat gcc ttt tct cta cag cac aac

Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln His Asn

145 150 155 160

tat ctt ttc aca gct ttt gaa gag aat tct tct aaa gga aat ggc gga

Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn Gly Gly

165 170 175

gcc att cag gct caa acc ttc tct tta tct aga aat gtg tcg cct att

Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser Pro Ile

180 185 190

tct ttc gcc cgt aat cgt gcg gat tta aat ggc ggc gct att tgc tgt

Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile Cys Cys

195 200 205

48 96 144 192 240 288 336 384 432 480 528 576 624

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210 215 220	
aac tcc gcc acg aat gga ggc gct att tgt tgt atc agc gat cta aac Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp Leu Asn	720
225 230 235 240	
acc tca gaa aaa ggc tct ctc tct gct tgt aac caa gaa acg cta Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu Thr Leu	768
245 250 255	
ttt gca agc aat tct gct aaa gaa aaa ggc ggg gct att tat gcc aag Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr Ala Lys	816
260 265 270	
cac atg gta ttg cgt tat aac ggt cct gtt tcc ttc att aac aac agc His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn Asn Ser	864
275 280 285	
gct aaa ata ggt gga gct atc gcc atc cag tcc gga ggg agt ctc tct Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser Leu Ser	912
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atc ctt gca ggt gaa gga tct gtt ctg ttc cag aat aac tcc caa cgc Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser Gln Arg	960
305 310 315 320	
acc tcc gac caa ggt cta gta aga aac gcc atc tac tta gag aaa gat Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Glu Lys Asp	1008
325 330 335	
gcg att ctt tct tcc tta gaa gct cgc aac gga gat att ctt ttc ttt Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu Phe Phe	1056
340 345 350	
gat cct att gta caa gaa agt agc agc aaa gaa tcg cct ctt ccc tcc Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser Pro Leu Pro Ser	1104
355 360 365	
tct ttg caa gcc agc gtg act tct ccc acc cca gcc acc gca tct cct Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala Ser Pro	1152
370 375 380	
tta gtt att cag aca agt gca aac cgt tca gtg att ttc tcg agc gaa Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser Ser Glu	1200
385 390 395 400	
cgt ctt tct gaa gaa gaa aaa act cct gat aac ctc act tcc caa cta Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser Gln Leu	1248
405 410 415	
cag cag cct atc gaa ctg aaa tcc gga cgc tta gtt tta aaa gat cgc Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys Asp Arg	1296
420 425 430	

gct gtc ctt tcc gcg cct tct ctc tct cag gat cct caa gct ctc ctc Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala Leu Leu 435 440 445	1344
att atg gaa gcg gga act tct tta aaa act tcc tct gat ttg aag tta Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu Lys Leu 450 455 460	1392
gct acg cta agt att ccc ctt cat tcc tta gat act gaa aaa agc gta Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys Ser Val 465 470 475 480	1440
act atc cac gcc cct aac ctt tct atc caa aag atc ttc ctc tct aat Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu Ser Asn 485 490 495	1488
tct gga gat gag aat ttt tat gaa aat gta gag ctt ctc agt aaa gag Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Leu Ser Lys Glu 500 505 510	1536
caa aac aat att cct ctc ctt act ctc tct aaa gag caa tct cat tta Gln Asn Asn Ile Pro Leu Leu Thr Leu Ser Lys Glu Gln Ser His Leu 515 520 525	1584
cat ctt cct gat ggg aac ctc tct tct cac ttt gga tat caa gga gat His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln Gly Asp 530 535 540	1632
tgg act ttt tct tgg aaa gat tct gat gaa ggg cat tct ctg att gct Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu Ile Ala 545 550 555 560	1680
aat tgg acg cct aaa aac tat gtg cct cat cca gaa cgt caa tct aca Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln Ser Thr 565 570 575	1728
ctc gtt gcg aac act ctt tgg aac acc tat tcc gat atg caa gct gtg Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln Ala Val 580 585 590	1776
cag tcg atg att aat aca ata gcg cac gga gga gcc tat cta ttt gga Gln Ser Met Ile Asn Thr Ile Ala His Gly Gly Ala Tyr Leu Phe Gly 595 600 605	1824
acg tgg gga tct gct gtt tct aat tta ttc tat gct cac gac agc tct Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Ala His Asp Ser Ser 610 615 620	1872
ggg aaa cct atc gat aat tgg cat cat aga agc ctt ggc tac cta ttc Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr Leu Phe 625 630 635 640	1920
ggt atc agt act cac agt tta gat gac cat tct ttc tgc ttg gct gca Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu Ala Ala 645 650 655	1968

gga caa tta ctc ggg aaa tcg tcc gat tcc ttt att acg tct aca gaa Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser Thr Glu 660 665 670	2016
acg acc tcc tat ata gct act gta caa gcg caa ctc gct acc tct cta Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr Ser Leu 675 680 685	2064
atg aaa atc tct gca cag gca tgc tac aat gaa agt atc cat gag cta Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His Glu Leu 690 695 700	2112
aaa aca aaa tat cgc tcc ttc tct aaa gaa gga ttc gga tcc tgg cat Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser Trp His 705 710 715 720	2160
agc gtt gca gta tcc gga gaa gtg tgc gca tcg att cct att gta tcc Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile Val Ser 725 730 735	2208
aat ggt tcc gga ctg ttc agc tcc tct att ttc tct aaa ctg caa Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys Leu Gln 740 745 750	2256
gga ttt tca gga aca cag gac ggt ttt gag gag agt tcg gga gag att Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly Glu Ile 755 760 765	2304
cgg tcc ttt tct gcc agc tct ttc aga aat att tca ctt cct ata gga Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro Ile Gly 770 775 780	2352
ata aca ttt gaa aaa aaa tcc caa aaa aca cga acc tac tat tac ttt Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr Tyr Phe 785 790 795 800	2400
cta gga gcc tac atc caa gac ctg aaa cgt gat gtg gaa tcg gga cct Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser Gly Pro 805 810 815	2448
gta gtg tta ctc aaa aat gcc gtc tcc tgg gat gct cct atg gcg aac Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met Ala Asn 820 825 830	2496
ttg gat tca cga gcc tac atg ttc agg ctt acg aat caa aga gct cta Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg Ala Leu 835 840 845	2544
cac aga ctt cag acg ctg tta aat gtg tct tgt gtg ctg cgt ggg caa His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg Gly Gln 850 855 860	2592
agc cat agt tac tcc ctg gat ctg ggg acc act tac agg ttc Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe 865 870 875	2634
tag	2637

<210> 4  
<211> 878  
<212> PRT  
<213> Chlamydia sp

<400> 4  
Met Arg Pro Asp His Met Asn Phe Cys Cys Leu Cys Ala Ala Ile Leu  
1 5 10 15  
Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu Gly Glu Thr Ala  
20 25 30  
Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe Glu Asp  
35 40 45  
Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala Ser Gln  
50 55 60  
Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe Val Ser  
65 70 75 80  
Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu Lys Gly  
85 90 95  
Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp Cys Ser  
100 105 110  
Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly Gln Leu  
115 120 125  
Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His Ala Glu  
130 135 140  
Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln His Asn  
145 150 155 160  
Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn Gly Gly  
165 170 175  
Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser Pro Ile  
180 185 190  
Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile Cys Cys  
195 200 205  
Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe Thr Gly  
210 215 220  
Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp Leu Asn  
225 230 235 240  
Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu Thr Leu  
245 250 255  
Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr Ala Lys  
260 265 270  
His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn Asn Ser  
275 280 285  
Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser Leu Ser  
290 295 300  
Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser Gln Arg  
305 310 315 320  
Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Glu Lys Asp  
325 330 335  
Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu Phe Phe  
340 345 350  
Asp Pro Ile Val Gln Glu Ser Ser Lys Glu Ser Pro Leu Pro Ser  
355 360 365  
Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala Ser Pro  
370 375 380  
Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser Ser Glu  
385 390 395 400  
Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser Gln Leu  
405 410 415

Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys Asp Arg  
           420                  425                  430  
 Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala Leu Leu  
           435                  440                  445  
 Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu Lys Leu  
           450                  455                  460  
 Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys Ser Val  
           465                  470                  475                  480  
 Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu Ser Asn  
           485                  490                  495  
 Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Leu Ser Lys Glu  
           500                  505                  510  
 Gln Asn Asn Ile Pro Leu Leu Thr Leu Ser Lys Glu Gln Ser His Leu  
           515                  520                  525  
 His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln Gly Asp  
           530                  535                  540  
 Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu Ile Ala  
           545                  550                  555                  560  
 Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln Ser Thr  
           565                  570                  575  
 Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln Ala Val  
           580                  585                  590  
 Gln Ser Met Ile Asn Thr Ile Ala His Gly Gly Ala Tyr Leu Phe Gly  
           595                  600                  605  
 Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Ala His Asp Ser Ser  
           610                  615                  620  
 Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr Leu Phe  
           625                  630                  635                  640  
 Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu Ala Ala  
           645                  650                  655  
 Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser Thr Glu  
           660                  665                  670  
 Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr Ser Leu  
           675                  680                  685  
 Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His Glu Leu  
           690                  695                  700  
 Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser Trp His  
           705                  710                  715                  720  
 Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile Val Ser  
           725                  730                  735  
 Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys Leu Gln  
           740                  745                  750  
 Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly Glu Ile  
           755                  760                  765  
 Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro Ile Gly  
           770                  775                  780  
 Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr Tyr Phe  
           785                  790                  795                  800  
 Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser Gly Pro  
           805                  810                  815  
 Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met Ala Asn  
           820                  825                  830  
 Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg Ala Leu  
           835                  840                  845  
 His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg Gly Gln  
           850                  855                  860  
 Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe  
           865                  870                  875

<210> 5  
<211> 42  
<212> PRT  
<213> Chlamydia sp

<400> 5  
Ser Gly Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn  
1 5 10 15  
Ser Val Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu  
20 25 30  
Thr Gly Asp Thr His Asn Leu Thr Asn Cys  
35 40

<210> 6  
<211> 107  
<212> PRT  
<213> Chlamydia sp

<400> 6  
Ser Gly Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn  
1 5 10 15  
Ser Val Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu  
20 25 30  
Thr Gly Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg  
35 40 45  
Tyr Ile Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val  
50 55 60  
Thr Ile Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile  
65 70 75 80  
Tyr Phe Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr  
85 90 95  
Ala Ser Pro Asn Ser Pro Thr Val Glu Ile Arg  
100 105

<210> 7  
<211> 81  
<212> PRT  
<213> Chlamydia sp

<400> 7  
Ser Leu Thr Gly Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn  
1 5 10 15  
Leu Arg Tyr Ile Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala  
20 25 30  
Ala Val Thr Ile Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu  
35 40 45  
Gly Ile Tyr Phe Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile  
50 55 60  
Gly Tyr Ala Ser Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile  
65 70 75 80  
Gly

<210> 8  
<211> 66  
<212> PRT  
<213> Chlamydia sp

<400> 8  
Gly Pro Val Ile Phe Glu Asn Asn Thr Cys Cys Arg Pro Phe Thr Ser  
1 5 10 15  
Ser Asn Pro Asn Ala Ala Val Asn Lys Ile Arg Glu Gly Gly Ala Ile  
20 25 30  
His Ala Gln Asn Leu Tyr Ile Asn His Asn His Asp Val Val Gly Phe  
35 40 45  
Met Lys Asn Phe Ser Tyr Val Arg Gly Gly Ala Ile Ser Thr Ala Asn  
50 55 60  
Thr Phe  
65

<210> 9  
<211> 67  
<212> PRT  
<213> Chlamydia sp

<400> 9  
Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr Asn  
1 5 10 15  
Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe  
20 25 30  
Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala  
35 40 45  
Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly  
50 55 60  
Asn Ile Val  
65

<210> 10  
<211> 92  
<212> PRT  
<213> Chlamydia sp

<400> 10  
Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg Leu  
1 5 10 15  
Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr  
20 25 30  
Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp  
35 40 45  
Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly  
50 55 60  
Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg  
65 70 75 80  
His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn  
85 90

<210> 11  
<211> 66  
<212> PRT  
<213> Chlamydia sp

<400> 11  
Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala Ser Ser  
1 5 10 15  
Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu Ile Phe  
20 25 30

Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser Phe Asn  
35 40 45  
Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala Thr Val  
50 55 60  
Asn Ser  
65

<210> 12  
<211> 51  
<212> PRT  
<213> Chlamydia sp

<400> 12  
Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr Pro Ala Pro  
1 5 10 15  
Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His Ala Gln Leu  
20 25 30  
Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser Leu Gly Asn  
35 40 45  
Gly Ala Val  
50

<210> 13  
<211> 66  
<212> PRT  
<213> Chlamydia sp

<400> 13  
Glu Ile Pro Leu Leu Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr  
1 5 10 15  
Thr Ala Asp Thr Ala Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser  
20 25 30  
Leu Ile Asp Asp Tyr Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr  
35 40 45  
His Ala Leu Ser Ser Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp  
50 55 60  
Asn Gln  
65

<210> 14  
<211> 36  
<212> PRT  
<213> Chlamydia sp

<400> 14  
Gln Leu Arg Ser Asp Asp Met Asp Phe Ser Gly Leu Asn Val Pro His  
1 5 10 15  
Tyr Gly Trp Gln Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp  
20 25 30  
Pro Glu Pro Ala  
35

<210> 15  
<211> 36  
<212> PRT  
<213> Chlamydia sp

<400> 15

Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala Thr Ile  
 1 5 10 15  
 Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu Leu Thr  
 20 25 30  
 Trp Leu Pro Ala  
 35

<210> 16  
 <211> 76  
 <212> PRT  
 <213> Chlamydia sp

<400> 16  
 Ala Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His  
 1 5 10 15  
 Arg Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro  
 20 25 30  
 Lys His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu  
 35 40 45  
 Leu Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Asp  
 50 55 60  
 His Pro Phe Trp Gly Ile Thr Gly Gly Leu Gly  
 65 70 75

<210> 17  
 <211> 76  
 <212> PRT  
 <213> Chlamydia sp

<400> 17  
 Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe Ser Gln Thr  
 1 5 10 15  
 Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val Ser Ser Lys  
 20 25 30  
 Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln Glu Gly Phe  
 35 40 45  
 Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp His Asn Cys  
 50 55 60  
 His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser  
 65 70 75

<210> 18  
 <211> 21  
 <212> PRT  
 <213> Chlamydia sp

<400> 18  
 Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln Glu  
 1 5 10 15  
 Gly Phe Leu Leu Thr  
 20

<210> 19  
 <211> 61  
 <212> PRT  
 <213> Chlamydia sp

<400> 19

Asp	His	Asn	Cys	His	His	Phe	Tyr	Thr	Gln	Gly	Glu	Asn	Leu	Thr	Ser
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Gln	Gly	Thr	Phe	Arg	Ser	Gln	Thr	Met	Gly	Gly	Ala	Val	Phe	Phe	Asp
								20	25				30		
Leu	Pro	Met	Lys	Pro	Phe	Gly	Ser	Thr	His	Ile	Leu	Thr	Ala	Pro	Phe
								35	40			45			
Leu	Gly	Ala	Leu	Gly	Ile	Tyr	Ser	Ser	Leu	Ser	His	Phe			
								50	55			60			
<210> 20															
<211> 51															
<212> PRT															
<213> Chlamydia sp															
<400> 20															
Phe	Asp	Leu	Pro	Met	Lys	Pro	Phe	Gly	Ser	Thr	His	Ile	Leu	Thr	Ala
1					5				10					15	
Pro	Phe	Leu	Gly	Ala	Leu	Gly	Ile	Tyr	Ser	Ser	Leu	Ser	His	Phe	Thr
							20		25			30			
Glu	Val	Gly	Ala	Tyr	Pro	Arg	Ser	Phe	Ser	Thr	Lys	Thr	Pro	Leu	Ile
					35			40			45				
Asn	Val	Leu													
		50													
<210> 21															
<211> 31															
<212> PRT															
<213> Chlamydia sp															
<400> 21															
Met	Lys	Lys	Ala	Phe	Phe	Phe	Leu	Ile	Gly	Asn	Ser	Leu	Ser	Gly	
1					5				10					15	
Leu	Ala	Arg	Glu	Val	Pro	Ser	Arg	Ile	Phe	Leu	Met	Pro	Asn	Ser	
					20				25			30			
<210> 22															
<211> 500															
<212> PRT															
<213> Chlamydia sp															
<400> 22															
Met	Lys	Lys	Ala	Phe	Phe	Phe	Leu	Ile	Gly	Asn	Ser	Leu	Ser	Gly	
1					5				10					15	
Leu	Ala	Arg	Glu	Val	Pro	Ser	Arg	Ile	Phe	Leu	Met	Pro	Asn	Ser	
					20				25			30			
Pro	Asp	Pro	Thr	Lys	Glu	Ser	Leu	Ser	Asn	Lys	Ile	Ser	Leu	Thr	Gly
				35			40			45					
Asp	Thr	His	Asn	Leu	Thr	Asn	Cys	Tyr	Leu	Asp	Asn	Leu	Arg	Tyr	Ile
				50			55			60					
Leu	Ala	Ile	Leu	Gln	Lys	Thr	Pro	Asn	Glu	Gly	Ala	Ala	Val	Thr	Ile
				65			70			75			80		
Thr	Asp	Tyr	Leu	Ser	Phe	Phe	Asp	Thr	Gln	Lys	Glu	Gly	Ile	Tyr	Phe
					85				90			95			
Ala	Lys	Asn	Leu	Thr	Pro	Glu	Ser	Gly	Gly	Ala	Ile	Gly	Tyr	Ala	Ser
				100			105			110					
Pro	Asn	Ser	Pro	Thr	Val	Glu	Ile	Arg	Asp	Thr	Ile	Gly	Pro	Val	Ile
				115			120			125					

Phe Glu Asn Asn Thr Cys Cys Arg Pro Phe Thr Ser Ser Asn Pro Asn  
 130 135 140  
 Ala Ala Val Asn Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn  
 145 150 155 160  
 Leu Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe  
 165 170 175  
 Ser Tyr Val Arg Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val  
 180 185 190  
 Ser Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln  
 195 200 205  
 Thr Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn  
 210 215 220  
 Ser Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys  
 225 230 235 240  
 Cys Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn  
 245 250 255  
 Arg Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu  
 260 265 270  
 Thr Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr  
 275 280 285  
 Arg Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn  
 290 295 300  
 Ile Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu  
 305 310 315 320  
 Val Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys  
 325 330 335  
 Gly Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala  
 340 345 350  
 Asp Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr  
 355 360 365  
 Asn Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala  
 370 375 380  
 Ile Thr Val Ala Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser  
 385 390 395 400  
 Ser Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly  
 405 410 415  
 Val Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val  
 420 425 430  
 Phe Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu  
 435 440 445  
 Gln Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys  
 450 455 460  
 Ile Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly  
 465 470 475 480  
 Gly Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn  
 485 490 495  
 Gly Ala Gly Asn  
 500

<210> 23  
 <211> 28  
 <212> PRT  
 <213> Chlamydia sp

<400> 23

Ala Ala Ile Leu Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu  
 1 5 10 15

Gly Glu Thr Ala Leu Leu Thr Lys Asn Pro Asn His  
                   20                      25  
  
 <210> 24  
 <211> 41  
 <212> PRT  
 <213> Chlamydia sp  
  
 <400> 24  
 Val Leu Gly Asn Ser Tyr Cys Trp Phe Val Ser Lys Leu His Ile Thr  
   1                  5                  10                  15  
 Asp Pro Lys Glu Ala Leu Phe Lys Glu Lys Gly Asp Leu Ser Ile Gln  
   20                  25                  30  
 Asn Phe Arg Phe Leu Ser Phe Thr Asp  
   35                  40  
  
 <210> 25  
 <211> 76  
 <212> PRT  
 <213> Chlamydia sp  
  
 <400> 25  
 Ile Ser Ala Asp Ala Phe Ser Leu Gln His Asn Tyr Leu Phe Thr Ala  
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 Phe Glu Glu Asn Ser Ser Lys Gly Asn Gly Ala Ile Gln Ala Gln  
   20                  25                  30  
 Thr Phe Ser Leu Ser Arg Asn Val Ser Pro Ile Ser Phe Ala Arg Asn  
   35                  40                  45  
 Arg Ala Asp Leu Asn Gly Gly Ala Ile Cys Cys Ser Asn Leu Ile Cys  
   50                  55                  60  
 Ser Gly Asn Val Asn Pro Leu Phe Phe Thr Gly Asn  
   65                  70                  75  
  
 <210> 26  
 <211> 41  
 <212> PRT  
 <213> Chlamydia sp  
  
 <400> 26  
 Ala Cys Asn Gln Glu Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys  
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 Gly Gly Ala Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro  
   20                  25                  30  
 Val Ser Phe Ile Asn Asn Ser Ala Lys  
   35                  40  
  
 <210> 27  
 <211> 86  
 <212> PRT  
 <213> Chlamydia sp  
  
 <400> 27  
 Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala Ser Pro Leu  
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 Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser Ser Glu Arg  
   20                  25                  30  
 Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser Gln Leu Gln  
   35                  40                  45

Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys Asp Arg Ala  
50 55 60  
Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala Leu Leu Ile  
65 70 75 80  
Met Glu Ala Gly Thr Ser  
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<210> 28  
<211> 56  
<212> PRT  
<213> Chlamydia sp

<400> 28  
Glu Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser Gln  
1 5 10 15  
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Arg Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala Leu  
35 40 45  
Leu Ile Met Glu Ala Gly Thr Ser  
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<210> 29  
<211> 51  
<212> PRT  
<213> Chlamydia sp

<400> 29  
Pro Leu His Ser Leu Asp Thr Glu Lys Ser Val Thr Ile His Ala Pro  
1 5 10 15  
Asn Leu Ser Ile Gln Lys Ile Phe Leu Ser Asn Ser Gly Asp Glu Asn  
20 25 30  
Phe Tyr Glu Asn Val Glu Leu Leu Ser Lys Glu Gln Asn Asn Ile Pro  
35 40 45  
Leu Leu Thr  
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<210> 30  
<211> 56  
<212> PRT  
<213> Chlamydia sp

<400> 30  
Ser Asn Leu Phe Tyr Ala His Asp Ser Ser Gly Lys Pro Ile Asp Asn  
1 5 10 15  
Trp His His Arg Ser Leu Gly Tyr Leu Phe Gly Ile Ser Thr His Ser  
20 25 30  
Leu Asp Asp His Ser Phe Cys Leu Ala Ala Gly Gln Leu Leu Gly Lys  
35 40 45  
Ser Ser Asp Ser Phe Ile Thr Ser  
50 55

<210> 31  
<211> 66  
<212> PRT  
<213> Chlamydia sp

<400> 31

Ser Phe Ser Lys Glu Gly Phe Gly Ser Trp His Ser Val Ala Val Ser  
 1 5 10 15  
 Gly Glu Val Cys Ala Ser Ile Pro Ile Val Ser Asn Gly Ser Gly Leu  
 20 25 30  
 Phe Ser Ser Phe Ser Ile Phe Ser Lys Leu Gln Gly Phe Ser Gly Thr  
 35 40 45  
 Gln Asp Gly Phe Glu Glu Ser Ser Gly Glu Ile Arg Ser Phe Ser Ala  
 50 55 60  
 Ser Ser  
 65

<210> 32  
 <211> 61  
 <212> PRT  
 <213> Chlamydia sp

<400> 32

Ser Gly Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser  
 1 5 10 15  
 Leu Pro Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr  
 20 25 30  
 Tyr Tyr Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val  
 35 40 45  
 Glu Ser Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser  
 50 55 60

<210> 33  
 <211> 31  
 <212> PRT  
 <213> Chlamydia sp

<400> 33

Met Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln  
 1 5 10 15  
 Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val  
 20 25 30

<210> 34  
 <211> 500  
 <212> PRT  
 <213> Chlamydia sp

<400> 34

Met Arg Pro Asp His Met Asn Phe Cys Cys Leu Cys Ala Ala Ile Leu  
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 Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu Gly Glu Thr Ala  
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 Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe Glu Asp  
 35 40 45  
 Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala Ser Gln  
 50 55 60  
 Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe Val Ser  
 65 70 75 80  
 Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu Lys Gly  
 85 90 95  
 Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp Cys Ser  
 100 105 110

Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly Gln Leu  
     115                 120                 125  
 Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His Ala Glu  
     130                 135                 140  
 Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln His Asn  
     145                 150                 155                 160  
 Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn Gly Gly  
     165                 170                 175  
 Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser Pro Ile  
     180                 185                 190  
 Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile Cys Cys  
     195                 200                 205  
 Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe Thr Gly  
     210                 215                 220  
 Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp Leu Asn  
     225                 230                 235                 240  
 Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu Thr Leu  
     245                 250                 255  
 Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr Ala Lys  
     260                 265                 270  
 His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn Asn Ser  
     275                 280                 285  
 Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser Leu Ser  
     290                 295                 300  
 Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser Gln Arg  
     305                 310                 315                 320  
 Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Glu Lys Asp  
     325                 330                 335  
 Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu Phe Phe  
     340                 345                 350  
 Asp Pro Ile Val Gln Glu Ser Ser Lys Glu Ser Pro Leu Pro Ser  
     355                 360                 365  
 Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala Ser Pro  
     370                 375                 380  
 Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser Ser Glu  
     385                 390                 395                 400  
 Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser Gln Leu  
     405                 410                 415  
 Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys Asp Arg  
     420                 425                 430  
 Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala Leu Leu  
     435                 440                 445  
 Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu Lys Leu  
     450                 455                 460  
 Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys Ser Val  
     465                 470                 475                 480  
 Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu Ser Asn  
     485                 490                 495  
 Ser Gly Asp Glu  
     500

<210> 35  
 <211> 10  
 <212> PRT  
 <213> Chlamydia sp

<400> 35

Val Pro Asp Pro Thr Lys Glu Ser Leu Ser  
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<210> 36  
<211> 126  
<212> DNA  
<213> Chlamydia sp

<400> 36  
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cctacgaaag agtcgctatc aaataaaaatt agtttgacag gagacactca caatctcact 120  
aactgca 126

<210> 37  
<211> 321  
<212> DNA  
<213> Chlamydia sp

<400> 37  
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cctacgaaag agtcgctatc aaataaaaatt agtttgacag gagacactca caatctcact 120  
aactgctatc tcgataacct acgctacata ctggctattc tacaaaaaac tcccaatgaa 180  
ggagctgctg tcacaataac agattaccta agctttttt atacacaaaaa agaaggatt 240  
tattttgc当地 300  
aaaatctcac ccctgaaaat ggtgggtgcga ttgggttatgc gagtcccaat 321  
tctcctaccg tggagattcg t

<210> 38  
<211> 243  
<212> DNA  
<213> Chlamydia sp

<400> 38  
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ctggctattc tacaaaaaac tcccaatgaa ggagctgctg tcacaataac agattaccta 120  
agctttttt atacacaaaaa agaaggatt tattttgc当地 180  
ggtgggtgcga ttgggttatgc gagtcccaat tctcctaccg tggagattcg tgatacaata 240  
ggt 243

<210> 39  
<211> 198  
<212> DNA  
<213> Chlamydia sp

<400> 39  
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gcagctgta ataaaaataag agaaggcga gcattcatg ctcaaatct ttacataat 120  
cataatcatg atgtggcgg atttatgaag aactttctt atgtccgagg aggagccatt 180  
agtaccgcta ataccctt 198

<210> 40  
<211> 201  
<212> DNA  
<213> Chlamydia sp

<400> 40  
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ggtggcgtta tctatgctgg aacgagcaat tctttgaga gtaataactg cgatctctc 120  
tttatcaata acgcctgttg tgcaggagga gcgatcttct cccctatctg ttctctaaca 180

ggaaatcgta gtaacatcg t

201

<210> 41  
<211> 276  
<212> DNA  
<213> Chlamydia sp

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<400> 41
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aatcgtggta ggatcttttt tagtgacaat atcacaaaaaa attatggcg agctatttac     120
gctcctgttag ttaccctagt ggataatggc cctacctact ttataaacaa tatcgccaaat    180
aataaggggg gcgcstatcta tatagacgga accagcaact ccaaaaatttc tgccgaccgc   240
catgctatta ttttaatga aaatattgtg actaat                                276

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<210> 42  
<211> 198  
<212> DNA  
<213> Chlamydia sp
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<400> 42  
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ctattaggag cagggagtag caaaaattta attttttatg atccatttga agtttagcaat 120  
gcaggggtct ctgtgtcctt caataaggaa gctgatcaaa caggctctgt agtattttca 180  
qqaqctactq ttaattct 198

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<210> 43  
<211> 153  
<212> DNA  
<213> Chlamydia sp
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<400> 43  
tctgcagatt ttcatcaacg caattttacaa acaaaaaacac ctgcacccct tactctcagt 60  
aatggttttc tatgtatcga agatcatgct cagcttacag tgaatcgatt cacacaact 120  
gggggtgttg tttctcttgg gaatggagca gtt 153

<210> 44  
<211> 198  
<212> DNA  
<213> Chlamydia sp

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<400> 44
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gcagctacct tttcattaag tgatgtaaaa ctctcactca ttgatgacta tgggaattct 120
ccttatgaat ccacagatct aaccatgct ctgtcatcac agcctatgct atctatttct 180
gaggcttagtg ataaccag 198

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<210> 45  
<211> 108  
<212> DNA  
<213> Chlamydia sp

<400> 45  
cagctaagat ctgatgatat ggattttcg ggactaaatg tccctcatta tggatggcaa 60  
ggactttgga cttgggactg ggcaaaaact caagatccag aaccagca 108

<210> 46  
<211> 108  
<212> DNA

<213> Chlamydia sp		
<400> 46		
ggctggccaa aaactcaaga tccagaacca gcatttcag caacaatcac agatccacaa	60	
aaagccaata gattccatag aactttatta ctgacttggc ttccctgct	108	
<210> 47		
<211> 228		
<212> DNA		
<213> Chlamydia sp		
<400> 47		
gcatcttcag caacaatcac agatccacaa aaagccaata gattccatag aactttatta	60	
ctgacttggc ttccctgctgg gtatgttccct agccccaaac acagaagtcc cctcatagcg	120	
aataccttat gggggatat gctgcttgca acagaaagct taaaaaatag tgcagaactg	180	
acacacctgt atcatcctt ctggggatt acaggaggag gactaggc	228	
<210> 48		
<211> 228		
<212> DNA		
<213> Chlamydia sp		
<400> 48		
atgatagcag ggcagacaca cacttctca ttgaaattca gtcagaccta caccaaactc	60	
aatgagcggtt acgcaaaaaa caacgtatct tctaaaaatt actcatgccca aggagaaaatg	120	
ctttctcat tgcaagaagg tttcttgctg actaaattag ttgggcttta cagctatgga	180	
gaccataact gtcaccattt ctataccaa ggagaaaatc taacatctca agggacgttc	228	
<210> 49		
<211> 63		
<212> DNA		
<213> Chlamydia sp		
<400> 49		
tctaaaaatt actcatgccca aggagaaaatg ctttctcat tgcaagaagg tttcttgctg	60	
act	63	
<210> 50		
<211> 183		
<212> DNA		
<213> Chlamydia sp		
<400> 50		
gaccataact gtcaccattt ctataccaa ggagaaaatc taacatctca agggacgttc	60	
cgttgtcaaa cgatggagg tgctgtttt ttgtatctcc ctatgaaacc ctttggatca	120	
acgcataatac tgacagctcc ctttttaggt gctcttggta ttatcttag cctgtctcac	180	
ttt	183	
<210> 51		
<211> 153		
<212> DNA		
<213> Chlamydia sp		
<400> 51		
tttgatctcc ctatgaaacc ctttggatca acgcataatac tgacagctcc ctttttaggt	60	
gctcttggta ttatcttag cctgtctcac ttatcttagg tgggagccta tccgcgaagc	120	
ttttctacaa agactcctt gatcaatgtc cta	153	

<210> 52		
<211> 93		
<212> DNA		
<213> Chlamydia sp		
<400> 52		
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gttccttcta gaatcttct tatgccccac tca	93	
<210> 53		
<211> 1500		
<212> DNA		
<213> Chlamydia sp		
<400> 53		
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gttccttcta gaatcttct tatgccccac tcagttccag atcctacgaa agatcgcta	120	
tcaaataaaa tttagtttgc acggagacact cacaatctca ctaactgcta tctcgataac	180	
ctacgctaca tactggctat tctacaaaaa actcccaatg aaggagctgc tgtcacaata	240	
acagattacc taagctttt tgatacacaa aaagaaggta ttatatttgc aaaaaatctc	300	
acccctgaaa gtgggtgtgc gattggttat gcgagtcac attctctac cgtggagatt	360	
cgtgatacaa taggtcctgt aatcttgaa aataatactt gttcagacc atttacatcg	420	
agtaatccta atgcagctgt taataaaaata agagaaggcg gagccattca tgctaaaaat	480	
ctttacataa atcataatca tgatgtggtc ggatttatga agaacttttgc ttatgtccga	540	
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tttatggaca acatctgtat tcaaactaat acacggaa aagggtggcgc tatctatgct	660	
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tttagtgaca atatcacaaa aaattatggc ggagctattt acgcttcgtt agttacccta	960	
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tatatacgtc gaaaccagcaa ctccaaaatt tctgccgacc gccatgtat tatttttaat	1080	
gaaaatattt tgactaatgt aactaatgca aatggtagca gtacgtcagc taatcctcct	1140	
agaagaaaatg caataacagt agcaagctcc tctggtaaa ttctatttagg agcagggagt	1200	
agccaaaatt taattttttgc tgatcctatt gaagtttagca atgcaggggt ctctgtgtcc	1260	
ttcaataagg aagctgatca aacaggctct gtatgtt cagggactac tggtaatttct	1320	
gcagattttc atcaacgcaa tttacaaaca aaaacacctg cacccttac tctcagtaat	1380	
ggttttctat gtatcgaga tcatgctcag cttagtga atcgattcac acaaactggg	1440	
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<210> 54		
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<212> DNA		
<213> Chlamydia sp		
<400> 54		
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ctcctcacta aaaatcctaa tcat	84	
<210> 55		
<211> 123		
<212> DNA		
<213> Chlamydia sp		
<400> 55		
gtacttgaa attcctactg ttggttcgta tctaaactcc atatcacgga ccccaaagag	60	
gctcttttgc aagaaaaagg agatcttcc attcaaaact ttcgcttcct ttccttcaca	120	

<210> 56		
<211> 228		
<212> DNA		
<213> Chlamydia sp		
<400> 56		
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tcttctaaag gaaatggcg agccatttag gctcaaaccct tctcttatac tagaaatgtg	120	
tcgcctattt ctccggcccg taatcgtag gatttaaatg gcggcgctat ttgctgtagt	180	
aatcttattt gttcaggaa tgtaaacccct ctctttca ctggaaac	228	
<210> 57		
<211> 123		
<212> DNA		
<213> Chlamydia sp		
<400> 57		
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tatgccaagc acatggatt gcgttataac ggtcctgttt ctttcattaa caacagcgct	120	
aaa	123	
<210> 58		
<211> 258		
<212> DNA		
<213> Chlamydia sp		
<400> 58		
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agtgc当地 acc gttcagtgtat ttctcgagc gaacgtctt ctgaagaaga aaaaactcct	120	
gataacctca ctcccaact acagcagcct atcgaactga aatccggacg cttagttta	180	
aaagatcgcg ctgtccttc cgcccttct ctctctcagg atcctcaagc tctcctcatt	240	
atgaaagcgg gaacttct	258	
<210> 59		
<211> 168		
<212> DNA		
<213> Chlamydia sp		
<400> 59		
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<210> 60		
<211> 153		
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agtaaaagacg aaaacaatat tcctctcatt act	153	
<210> 61		
<211> 168		
<212> DNA		

<213> Chlamydia sp

<400> 61

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agccttggct acctattcgg tatcagactact cacagtttag atgaccatcc tttctgcttg	120
gctgcaggac aattactcgg gaaatcgccc gattccctta ttacgtct	168

<210> 62

<211> 198

<212> DNA

<213> Chlamydia sp

<400> 62

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gcatcgattc ctattgtatc caatgggtcc ggactgttca gctccttctc tattttctct	120
aaactgcaag gattttcagg aacacaggac gggtttgagg agagttcggg agagattcgg	180
tcctttctcg ccagctct	198

<210> 63

<211> 183

<212> DNA

<213> Chlamydia sp

<400> 63

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ataacatttg aaaaaaaaatc caaaaaaaaaca cgaacctact attacttctt aggaggctac	120
atccaagacc tgaaacgtga tgtggaatcg ggacctgttag tgttactcaa aaatgccgtc	180
tcc	183

<210> 64

<211> 93

<212> DNA

<213> Chlamydia sp

<400> 64

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<210> 65

<211> 1500

<212> DNA

<213> Chlamydia sp

<400> 65

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gtcgctgtatc catttttgc ggactgtacc atggagagcc tctttctgc tctttgtgt	180
catgcacatc aagacgtatcc ttgtatgtatc ctggaaatt cctactgttg gttcgatct	240
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caaaaacttgc gcttccttc cttcacagat tgcctttccaa agggaaagctc tccttcttatt	360
attcatcaaa agaatggtca gttatccttgc cgaataatag gtagcatgag tttctgtcga	420
aatcatgtcg aaggctctgg aggagccatc tctgcggat cttttctct acagcacaac	480
tatctttca cagctttgc agagaattct tctaaaggaa atggccggatc cattcaggct	540
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